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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/090,183

DATE: 03/20/2002

TIME: 11:34:49

Input Set : A:\TSRI8290SEQ.TXT

Output Set: N:\CRF3\03202002\J090183.raw

4 <110> APPLICANT: The Scripps Research Institute  
5 Ralph A. Reisfeld  
6 Andrew G. Niethammer  
7 Rong Xiang  
9 <120> TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING  
10 ENDOTHELIAL CELLS AND METHODS OF USE THEREOF  
13 <130> FILE REFERENCE: TSRI-829.0  
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/090,183  
C--> 15 <141> CURRENT FILING DATE: 2002-03-02  
15 <160> NUMBER OF SEQ ID NOS: 6  
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 4071  
21 <212> TYPE: DNA  
22 <213> ORGANISM: human  
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27 cttacaatta aggctaatac aactcttcaa attacttgca ggggacagag ggacttggac 180  
28 tggctttggc ccaataatca gaggggcagt gagcaaaggg tggaggtgac tgagtgcagc 240  
29 gatggcctct tctgtaagac actcacaatt ccaaaagtga tcggaaatga cactggagcc 300  
30 tacaagtgtc tctaccggga aactgacttg gcctcggtea tttatgtcta tgttcaagat 360  
31 tacagatctc catttattgc ttctgttagt gaccaacatg gagtcgtgta cttactgag 420  
32 aacaaaaaca aaactgtggt gattccatgt ctcggtcca tttcaaatct caacgtgtca 480  
33 ctttgtgcaa gatacccaga aaagagattt gttcctgatg gtaacagaat ttcttgggac 540  
34 agcaagaagg gctttactat tcccagctac atgatcagct atgctggcat ggtcttctgt 600  
35 gaagcaaaaa ttaatgatga aagttaccag tctattatgt acatagttgt cgttgtaggg 660  
36 tataggattt atgatgtggt tctgagtcgg tctcatggaa ttgaactatc tgttgagaaa 720  
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38 gaataccctt cttcgaagca tcagcataag aaacttgtaa accgagacct aaaaaccag 840  
39 tctgggagtg agatgaagaa atttttgagc accttaacta tagatggtgt aaccgggagt 900  
40 gaccaaggat tgtacacctg tgcagcatcc agtgggctga tgaccaagaa gaacagcaca 960  
41 tttgtcaggg tccatgaaaa accttttggt gcttttgaa gtggcatgga atctctggtg 1020  
42 gaagccacgg tgggggagcg tgtcagaatc cctgcgaagt accttggtta cccaccccca 1080  
43 gaaataaaat ggtataaaaa tggaaatccc ctgagtgcca atcacacaat taaagcgggg 1140  
44 catgtactga cgattatgga agtgagtga agagacacag gaaattacac tgtcatcctt 1200  
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50 aaaaatcaat ttgctcta atgaggaaaa aacaaaactg taagtaccct tgttatccaa 1560  
51 ggggcaaatg tgtcagcttt gtacaaatgt gaagcgggtc acaaagtcgg gagaggagag 1620

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55 cctgttttgca agaacttggg tactcttttg aaattgaatg ccaccatggt ctctaatagc 1860
56 acaaatgaca ttttgatcat ggagcttaag aatgcatact tgcaggacca aggagactat 1920
57 gtctgccttg ctcaagacag gaagaccaag aaaagacatt gcgtggtcag gcagctcaca 1980
58 gtcctagagc gtgtggcacc cacgatcaca ggaaacctgg agaatacagac gacaagtatt 2040
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62 agtgttcttg gctgtgcaaa agtggaggca tttttcataa tagaagggtg ccaggaaaag 2280
63 acgaacttgg aaatcattat tctagtaggc acggcgggtg ttgccatggt cttctggcta 2340
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90 cagacaagcg gctaccagtc cggatatcac tccgatgaca cagacaccac cgtgtactcc 3960
91 agtgaggaag cagaactttt aaagctgata gagattggag tgcaaaccgg tagcacagcc 4020
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94 &lt;210&gt; SEQ ID NO: 2

95 &lt;211&gt; LENGTH: 1356

96 &lt;212&gt; TYPE: PRT

97 &lt;213&gt; ORGANISM: human

99 &lt;400&gt; SEQUENCE: 2

100 Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu

101 1 5 10 15

102 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro

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103          20          25          30
104 Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
105          35          40          45
106 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
107          50          55          60
108 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
109 65          70          75          80
110 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
111          85          90          95
112 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
113          100          105          110
114 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
115          115          120          125
116 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
117          130          135          140
118 Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
119 145          150          155          160
120 Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
121          165          170          175
122 Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
123          180          185          190
124 Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
125          195          200          205
126 Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
127          210          215          220
128 Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
129 225          230          235          240
130 Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
131          245          250          255
132 Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
133          260          265          270
134 Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
135          275          280          285
136 Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
137          290          295          300
138 Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
139 305          310          315          320
140 Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
141          325          330          335
142 Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
143          340          345          350
144 Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
145          355          360          365
146 Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
147          370          375          380
148 Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
149 385          390          395          400
150 Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
151          405          410          415

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152 Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
153           420           425           430
154 Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
155           435           440           445
156 Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
157           450           455           460
158 Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
159 465           470           475           480
160 Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
161           485           490           495
162 Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
163           500           505           510
164 Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
165           515           520           525
166 Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
167           530           535           540
168 Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
169 545           550           555           560
170 Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
171           565           570           575
172 Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
173           580           585           590
174 Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
175           595           600           605
176 Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
177           610           615           620
178 Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
179 625           630           635           640
180 Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
181           645           650           655
182 Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
183           660           665           670
184 Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
185           675           680           685
186 Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
187           690           695           700
188 Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
189 705           710           715           720
190 Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
191           725           730           735
192 Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
193           740           745           750
194 Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu
195           755           760           765
196 Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Val Ile
197           770           775           780
198 Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly
199 785           790           795           800
200 Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His

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201                805                810                815
202 Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp
203                820                825                830
204 Arg Leu Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val
205                835                840                845
206 Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr
207                850                855                860
208 Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg
209 865                870                875                880
210 Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu
211                885                890                895
212 Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu
213                900                905                910
214 Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu
215                915                920                925
216 Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
217                930                935                940
218 Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
219 945                950                955                960
220 Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
221                965                970                975
222 Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro
223                980                985                990
224 Glu Asp Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr
225                995                1000                1005
226 Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys
227                1010                1015                1020
228 Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn
229 1025                1030                1035                1040
230 Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp
231                1045                1050                1055
232 Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met
233                1060                1065                1070
234 Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val
235                1075                1080                1085
236 Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser
237                1090                1095                1100
238 Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys
239 1105                1110                1115                1120
240 Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr
241                1125                1130                1135
242 Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr
243                1140                1145                1150
244 Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala
245                1155                1160                1165
246 Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu
247                1170                1175                1180
248 Ser Met Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser
249 1185                1190                1195                1200

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VERIFICATION SUMMARY

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Input Set : A:\TSRI8290SEQ.TXT

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date